```
   GAATTCGGCACGAGGTTTTTTTTTTTTTTTCCCCTCTTTCTTTCTTTTCCTTTGCC
1  ---------+---------+---------+---------+---------+---------+ 60

   ATCCGAAAGAGCTGTCAGCCGCCGCCGGGCTGCACCTAAAGGCGTCGGTAGGGGGATAAC
61 ---------+---------+---------+---------+---------+---------+ 120

   AGTCAGAGACCCTCCTGAAAGCAGGAGACGGGACGGTACCCCTCCGGCTCTGCGGGGCGG
121 ---------+---------+---------+---------+---------+---------+ 180

   CTGCGGCCCCTCCGTTCTTTCCCCCTCCCCGAGAGACACTCTTCCTTTCCCCCCACGAAG
181 ---------+---------+---------+---------+---------+---------+ 240

   ACACAGGGGCAGGAACGCGAGCGCTGCCCCTCCGCCATGGGAGGCCGCTTCCTGCTGACG
241 ---------+---------+---------+---------+---------+---------+ 300
```

FIG. 1A

```
                                                                    CTCGCCCTCCTCTCGGCGCTGCTGTGCCGCTGCCAGGTTGACGGCTCCGGGGTGTTCGAG
301 ---------+---------+---------+---------+---------+---------+---------+ 360

                                                                    CTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGGCTGCTCAGCAACCGCAACTGCTGCCGG
361 ---------+---------+---------+---------+---------+---------+---------+ 420

                                                                    GGGGGCGGCCCCGGAGGCGCCGGGCAGCAGCAGTGCGACTGCAAGACCTTCTTCCGCGTC
421 ---------+---------+---------+---------+---------+---------+---------+ 480

                                                                    TGCCTGAAGCACTACCAGGCCAGCGTCTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCC
481 ---------+---------+---------+---------+---------+---------+---------+ 540

                                                                    ATCACCCCCGTCCTCGGCGCCAACTCCTTCAGCGTCCCCGACGGCGCGGGCGGCGCCGAC
541 ---------+---------+---------+---------+---------+---------+---------+ 600

                                                                    CCCGCCTTCAGCAACCCCATCCGCTTCCCCTTCGGCTTCACCTGGCCCGGCACCTTCTCG
601 ---------+---------+---------+---------+---------+---------+---------+ 660

                                                                    CTCATCATCGAGGCTCTGCACACCGACTCCCCCGACGACCTCACCACAGAAAACCCCGAG
661 ---------+---------+---------+---------+---------+---------+---------+ 720
```

FIG. 1A (cont'd)

```
                                                                    780
    CGCCTCATCAGCCGCCTGGCCACCCAGAGGCACCTGGCGGTGGGCGAGGAGTGGTCCCAG
721 ---------+---------+---------+---------+---------+---------+

                                                                    840
    GACCTGCACAGCAGCGGCCGCACCGACCTCAAGTACTCCTATCGCTTTGTGTGTGATGAG
781 ---------+---------+---------+---------+---------+---------+

                                                                    900
    CACTACTACGGGGAAGGCTGCTCTGTCTTCTGCCGGCCCCGTGACGACCGCTTCGGTCAC
841 ---------+---------+---------+---------+---------+---------+

                                                                    960
    TTCACCTGTGGAGAGCGTGGCGAGAAGGTCTGCAACCCAGGCTGGAAGGGCCAGTACTGC
901 ---------+---------+---------+---------+---------+---------+

                                                                   1020
    ACTGAGCCGATTTGCTTGCCTGGGTGTGACGAGCAGCACGGCTTCTGCGACAAACCTGGG
961 ---------+---------+---------+---------+---------+---------+

                                                                   1080
    GAATGCAAGTGCAGAGTGGGTTGGCAGGGGCGGTACTGTGACGAGTGCATCCGATACCCA
1021 ---------+---------+---------+---------+---------+---------+

                                                                   1140
    GGCTGCCTGCACGGTACCTGTCAGCAGCCATGGCAGTGCAACTGCCAGGAAGGCTGGGGC
1081 ---------+---------+---------+---------+---------+---------+
```

FIG. 1A (cont'd)

```
                GGCCTTTTCTGCAACCAGGACCTGAACTACTGCACTCACCACAAGCCATGCAAGAATGGT
1141 ---------+---------+---------+---------+---------+---------+ 1200

1201 ---------+---------+---------+---------+---------+---------+ 1260
     CGGTGTACGTGGTTGTGGCCAGTCCCCTCCATGTGAACAAGAACGGCTGGACCCATGTGT

                GGCTCCAGCTGCGAGATTGAAATCAACGAATGTGATGCCAACCCTTGCAAGAATGGTGGA
1261 ---------+---------+---------+---------+---------+---------+ 1320

                AGCTGCACGGATCTCGAGAACAGCTATTCCTGTACCTGCCCCCCAGGCTTCTATGGTAAA
1321 ---------+---------+---------+---------+---------+---------+ 1380

                AACTGTGAGCTGAGTGCAATGACTTGTGCTGATGGACCGTGCTTCAATGGAGGGCGATGC
1381 ---------+---------+---------+---------+---------+---------+ 1440

                ACTGACAACCCTGATGGTGGATACAGCTGCCGCTGCCCACTGGGTTATTCTGGGTTCAAC
1441 ---------+---------+---------+---------+---------+---------+ 1500

                TGTGAAAAGAAAATCGATTACTGCAGTTCCAGCCCTTGTGCTAATGGAGCCCAGTGCGTT
1501 ---------+---------+---------+---------+---------+---------+ 1560
```

FIG. 1A (cont'd)

```
      GACCTGGGGAACTCCTACATATGCCAGTGCCAGGCTGGCTTCACTGGCAGGCACTGTGAC
1561  ---------+---------+---------+---------+---------+---------+ 1620

      GACAACGTGGACGATTGCGCCTCCTTCCCCTGCGTCAATGGAGGGACCTGTCAGGATGGG
1621  ---------+---------+---------+---------+---------+---------+ 1680

      GTCAACGACTACTCCTGCACCTGCCCCCCGGGATACAACGGGAAGAACTGCAGCACGCCG
1681  ---------+---------+---------+---------+---------+---------+ 1740

      GTGAGCAGATGCGAGCACAACCCCTGCCACAATGGGGCCACCTGCCACGAGAGAAGCAAC
1741  ---------+---------+---------+---------+---------+---------+ 1800

      CGCTACGTGTGCGAGTGCGCTCGGGGCTACGGCGGCCTCAACTGCCAGTTCCTGCTCCCC
1801  ---------+---------+---------+---------+---------+---------+ 1860

      GAGCCACCTCAGGGGCCGGTCATCGTTGACTTCACCGAGAAGTACACAGAGGGCCAGAAC
1861  ---------+---------+---------+---------+---------+---------+ 1920

      AGCCAGTTTCCCTGGATCGCAGTGTGCGCCGGGATTATTCTGGTCCTCATGCTGCTGCTG
1921  ---------+---------+---------+---------+---------+---------+ 1980
```

FIG. 1A (cont'd)

```
                TACCAGTCGGTGTACGTCATATCAGAAGAGAAAGATGAGTGCATCATAGCAACTGAGGTG
2401 ----------+----------+----------+----------+----------+----------+ 2460

                TAAAACAGACGTGACGTGGCAAAGCTTATCGATACCGTCATCAAGCTT
2461 ----------+----------+----------+----------+----------+-------- 2508
```

FIG. 1A (cont'd)

```
1 GAATTCGGCACGAGGTTTTTTTTTTTTTTTTCCCCTCTTTCTTTCTTTTCCTTTGCCATCCGAAAG  69

70 AGCTGTCAGCCGCCGCCGGGCTGCACCTAAAGGCGTCGGTAGGGGATAACAGTCAGAGACCCTCCTGA 138

139 AAGCAGGAGACGGGACGGTACCCCTCCGGCTCTGCGGGCCGGCTGCGGCCCCTCCGTTCTTTCCCCCTC 207

208 CCCGAGAGACACTCTTCCTTTCCCCCCACGAAGACACAGGGGCAGGAACGCGAGCGCTGCCCCTCCGCC 276

277 ATGGGAGGCCGCTTCCTGCTGACGCTCGCCCTCCTCTCGGCGCTGCTGTGCCGCTGCCAGGTTGACGGC 345

346 TCCGGGGTGTTCGAGCTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGGCTGCTCAGCAACCGCAACTGC 414

415 TGCCGGGGGGGGCGGCCCCGGAGGCGCCGGGCAGCAGCAGTGCGACTGCAAGACCTTCTTCCGCGTCTGC 483
```

FIG. 1B

484 CTGAAGCACTACCAGGCCAGCGTCTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCCAT

553 CTCGGCGCCAACTCCTTCAGCGTCCCCGACGGCGCGGGCGGCGCCGACCCCGCCTTCA

622 CGCTTCCCCTTCGGCTTCACCTGGCCCGGCACCTTCTCGCTCATCATCGAGGCTCTGC

691 CCCGACGACCTCACCACAGAAAACCCCGAGCGCCTCATCAGCCGCCTGGCCACCCAGA

760 GTGGGCGAGGAGTGGTCCCAGGACCTGCACAGCAGCGGCCGCACCGACCTCAAGTAC

FIG. 1B (cont'd)

GTGTGATGAGCACTACTACGGCGAAGGCTGCTCTGTCTTCTGCCGGCCCCGTGACGACCGCTTCGGT 897

898(CACTTCACCTGTGGAGAGCGTGGCGAGAAGGTCTGCAACCCAGGCTGGAAGGGCCAGTACTGCACTGAG 966

967 CCGATTTGCTTGCCTGGGTGTGACGAGCAGCACGGCTTCTGCGACAAACCTGGGGAATGCAAGTGCAGA 1035

1036 GTGGGTTGGCAGGGGCGGTACTGTGACGAGTGCATCCGATACCCAGGCTGCCTGCACGGTACCTGTCAG 1104

1105 CAGCCATGGCAGTGCAACTGCCAGGAAGGCTGGGGCGGCCTTTTCTGCAACCAGGACCTGAACTACTGC 1173

1174 ACTCACCACAAGCCATGCAAGAATGGTGCCACATGCACCAACACCGGTCAGGGGAGCTACACTTGTTCT 1242

1243 TGCCGACCTGGGTACACAGGCTCCAGCTGCGAGATTGAAATCAACGAATGTGATGCCAACCCTTGCAAG 1311

FIG. 1B (cont'd)

1312 AATGGTGGAAGCTGCACGGATCTCGAGAACAGCTATTCCTGTACCTGCCCCCCAGGCTTCTATGGTAAA 1380

1381 AACTGTGAGCTGAGTGCAATGACTTGTGCTGATGGACCGTGCTTCAATGGAGGGCGATGCACTGACAAC 1449

1450 CCTGATGGTGGATACAGCTGCCGCTGCCCACTGGGTTATTCTGGGTTCAACTGTGAAAAGAAAATCGAT 1518

1519 TACTGCAGTTCCAGCCCTTGTGCTAATGGAGCCCAGTGCGTTGACCTGGGGAACTCCTACATATGCCAG 1587

1588 TGCCAGGCTGGCTTCACTGGCAGGCACTGTGACGACAACGTGGACGATTGCGCCTCCTTCCCCTGCGTC 1656

1657 AATGGAGGGACCTGTCAGGATGGGGTCAACGACTACTCCTGCACCTGCCCCCCGGGATACAACGGGAAG 1725

FIG. 1B (cont'd)

1726 AACTGCAGCACGCCGGTGAGCAGATGCGAGCACAACCCCTGCCACAATGGGGCCACCTGCCACGAGAGA 1794

1795 AGCAACCGCTACGTGTGCGAGTGCGCTCGGGGCTACGGCGGCCTCAACTGCCAGTTCCTGCTCCCCGAG 1863

1864 CCACCTCAGGGGCCGGTCATCGTTGACTTCACCGAGAAGTACACAGAGGGCCAGAACAGCCAGTTTCCC 1932

1933 TGGATCGCAGTGTGCGCCGGGATTATTCTGGTCCTCATGCTGCTGCTGGGTTGCGCCGCCATCGTCGTC 2001

2002 TGCGTCAGGCTGAAGGTGCAGAAGAGGCACCATCAGCCCGAGGCCTGCAGGAGTGAAACGGAGACCATG 2070

2071 AACAACCTGGCGAACTGCCAGCGCGAGAAGGACATCTCCATCAGCGTCATCGGTGCCACTCAGATTAAA 2139

2140 AACACAAATAAGAAAGTAGACTTTCACAGCGATAACTCCGATAAAAACGGCTACAAAGTTAGATACCCA 2208

FIG. 1B (cont'd)

2209 TCAGTGGATTACAATTTGGTGCATGAACTCAAGAATGAGGACTCTGTGAAAGAGGAGCATGGCAAATGC 2277

2278 GAAGCCAAGTGTGAAACGTATGATTCAGAGGCAGAAGAGAAAAGCGCAGTACAGCTAAAAAGTAGTGAC 2346

2347 ACTTCTGAAAGAAAACGGCCAGATTCAGTATATTCCACTTCAAAGGACACAAAGTACCAGTCGGTGTAC 2415

2416 GTCATATCAGAAGAGAAAGATGAGTGCATCATAGCAACTGAGGTTAGTATCCCACCTGGCAGTCGGACA 2484

2485 AGTCTTGGTGTGTGATTCCCATCCAGCGCAGGTCAGGGCGGCCAAACCATTCTACCTGCTGCCACAGTC 2553

2554 ATCTGTACCCAATGAAAACTGGCCACCTTCAGTCTGTGGCACTGCAGACGTTGAAAAAACTTGTTGTGG 2622

FIG. 1B (cont'd)

2623 ATTAACATAAGCTCCAGTGGGGGTTACAGGGACAGCAATTTTTGCAGGCAAGGGTATAACTGTAGTGCA 2691

2692 GTTGTAGCTTACTAACCCTACTGACTCATTCTTTCGTGTGCTTCCTGCAGAGCCTGTTTTTGCTTGGCA 2760

2761 TTGAGGTGAAGTCCTGACCCTCTGCATCCTCATAGTCCTCTGCTTTCTTTTTATTAACCTCTTCTGGTC 2829

2830 TCTGCTTGTGTTTTCTCTCAACAGGTGTAAAACAGACGTGACGTGGCAAAGCTT 2883

FIG. 1B (cont'd)

```
  1 MGGRFLLTLA LLSALLCRCQ VDGSGVFELK LQEFVNKKGL LSNRNCCRGG GPGGAGQQQC
 61 DCKTFFRVCL KHYQASVSPE PPCTYGSAIT PVLGANSFSV PDGAGGADPA FSNPIRFPFG
121 FTWPGTFSLI IEALHTDSPD DLTTENPERL ISRLATQRHL AVGEEWSQDL HSSGRTDLKY
181 SYRFVCDEHY YGEGCSVFCR PRDDRFGHFT CGERGEKVCN PGWKGQYCTE PICLPGCDEQ
241 HGFCDKPGEC KCRVGWQGRY CDECIRYPGC LHGTCQQPWQ CNCQEGWGGL FCNQDLNYCT
301 HHKPCKNGAT CTNTGQGSYT CSCRPGYTGS SCEIEINECD ANPCKNGGSC TDLENSYSCT
361 CPPGFYGKNC ELSAMTCADG PCFNGGRCTD NPDGGYSCRC PLGYSGFNCE KKIDYCSSSP
421 CANGAQCVDL GNSYICQCQA GFTGRHCDDN VDDCASFPCV NGGTCQDGVN DYSCTCPPGY
481 NGKNCSTPVS RCEHNPCHNG ATCHERSNRY VCECARGYGG LNCQFLLPEP PQGPVIVDFT
541 EKYTEGQNSQ FPWIAVCAGI ILVLMLLLGC AAIVVCVRLK VQKRHHQPEA CRSETETMNN
601 LANCQREKDI SISVIGATQI KNTNKKVDFH SDNSDKNGYK VRYPSVDYNL VHELKNEDSV
661 KEEHGKCEAK CETYDSEAEE KSAVQLKSSD TSERKRPDSV YSTSKDTKYQ SVYVISEEKD
721 ECIIATEV
```

FIG. 2

```
C-Delta-1     1  MGGRFLLTLA-LLSALLCRCQVDGSGVPELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQQC 60
X-Delta-1     1  MGQQRMLTLL-VLSAVL--CQISCSGLFELRLQEFVNKKGLLGNMNCCRPGGSL--ASLQRC 56
Delta         1  --MHWIKCLLTAFICPTVIVQVHSSGSPELRLKYFSNDHGRDNEGRCCSGESDGATGKCLG  59

C-Delta-1    61  DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPPFGF 121
X-Delta-1    57  ECKTFFRICLKHYQSNVSPEPPCTYGGAVTPVLGTNSFVVPESS-SNADPTFSNPIRFPPFGF 116
Delta        60  SCKTRFRLCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPPFSF 120

C-Delta-1   122  TWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSY 182
X-Delta-1   117  TWPGTFSLIIEAIHADSADDLNTENPERLISRLATQRHLTVGEQWSQDLHSSDRTELKYSY 177
Delta       121  SWPGTFSLIVEAWH-DTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDF 180

C-Delta-1   183  RFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHGF 243
X-Delta-1   178  RFVCDEYYYGEGCSDYCRPRDDAFGHFSCGERGEKLCNPGWKGLYCTEPICLPGCDEHHGY 238
Delta       181  RVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCE--HGH 239
                                                  DSL

C-Delta-1   244  CDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKP 304
X-Delta-1   239  CDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTRHKP 299
Delta       240  CDKPNQCVCQLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRP 300
                 EGF1                                  EGF2

C-Delta-1   305  CKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDA--NPCKNGGSCTD---LENSYSCT 360
X-Delta-1   300  CENGATCTNTGQGSYTCSCRPGYTGSNCEIEVNECDA--NPCKNGGSCSD---LENSYTCS 355
Delta       301  CKNGGTCPNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCH 361
                 EGF3                                  EGF4

C-Delta-1   361  CPPGFYGKNCELSAMTCADGPCFNG-----GRCTDNPDGGYSCRCPLGYSGFNCEKKIDYC 416
X-Delta-1   356  CPPGFYGKNCELSAMTCADGPCPNG-----GRCADNPDGGYICFCPGVYSGFNCEKKIDYC 411
Delta       362  CRNGWSGKMCEEKVLTCSDKPCHQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDNC 422
                 EGF5

C-Delta-1   417  SSSPCANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCP 477
X-Delta-1   412  SSNPCANGARCEDLGNSYICQCQEGFSGRNCDDNLDDCTSFPCQNGGTCQDGINDYSCTCP 472
Delta       423  SPNPCINGGSCQPSGK---CICPSGFSGTRCETNIDDCLGHQCENGGTCIDMVNQYRCQCV 480
                 EGF6                                  EGF7

C-Delta-1   478  PGYNGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGP----- 534
X-Delta-1   473  PGYIGKNCSMPITKCEHNPCHNGATCHERNNRYVCQCARGYGGNNCQFLLPE---------- 524
Delta       481  PGFHGTHCSSKVDLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDCSVDIDECSSGPCHNG 541
                 EGF8

C-Delta-1   535  ----------------------------VIVDFTE--KYTEGQNSQFPW--IAVCAGIILVL 564
X-Delta-1   525  ----------------------------EKPVVVDLTE--KYTEGQSGQFPW--IAVCAGIVLVL 557
Delta       542  GTCMNRVNSFECVCANGFRGKQCDEESYDSVTFDAHQYGATTQARADGLANAQVVLIAVFS 602
                 EGF9

C-Delta-1   565  MLLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNNLANCQREKD--ISISVIGATQIKNT 623
X-Delta-1   558  MLLLGCAAVVVCVRVRVQKRRHQPEACRGESKTMNNLANCQREKD--ISVSFIGTTQIKNT 616
Delta       603  VAMPLVAVIAACVVFCMKRKRKRAQEKDNAEARKQNEQNAVATMHHNGSAVGVALASASMG 663
                 TM

C-Delta-1   624  NKKVDFHSD-NSDKNGYKVRYPSVDYNLVHELKNEDSVKEEHGKCEAKCETYDSEAEEKSA 683
X-Delta-1   617  NKKIDFLSESNNEKNGYKPRYPSVDYNLVHELKNEDSPKEERSKCEAKCSSNDSDSEDVNS 677
Delta       664  GKTGSNSGLTFDGGNPNIIKNTWDKSVN-NICASAAAAAAAAAAADECLMYGGYVASVADN 723

C-Delta-1   684  -----VQLKSSDTSERK---------RPDSVYSTSKDTKYQSVYVISEEKDECIIATEV 728
X-Delta-1   678  -----VHSK-RDSSERR---------RPDSAYSTSKDTKYQSVYVISDEKDECIIATEV 721
Delta       724  NNANSDFCVAPLQRAKSQKQLNTDPTLMHRGSPAGTSAKGASGGGPGAAEGKRISVLGEGS 784

Delta       785  YCSQRWPSLAAAGVAGACSSQLMAAASAAGTDGTAQQQRSVVCGTPHM               832
```

FIG. 3

```
C-Delta-1     184  V-CDEHYYGE G-CSVFCRPR DDRFGHFTCG ERGEKVCNPG WKGQYC  228
Delta         182  VTCDLNYYGS G-CAKFCRPR DDSFGHSTCS ETGEIICLTG WQGDYC  226
Serrate       235  VQCAVTYYNT TFCTTFCRPR DDQFGHYACG SEGQKLCLNG WQGVNC  279
C-Serrate-1        VTCAEHYYGF G-CNKFCRPR DDFFTHHTCD QNGNKTCLEG WTGPEC

apx-1         130  NLCSSNYHGK R-CNRYCIAN -AKLHWE-CS THGVRRCSAG WSGEDC  172
lag-2         120  VTCARNYFGN R-CENFCDAH LAKAARKRCD AMGRLRCDIG WMGPHC  166
```

FIG. 4

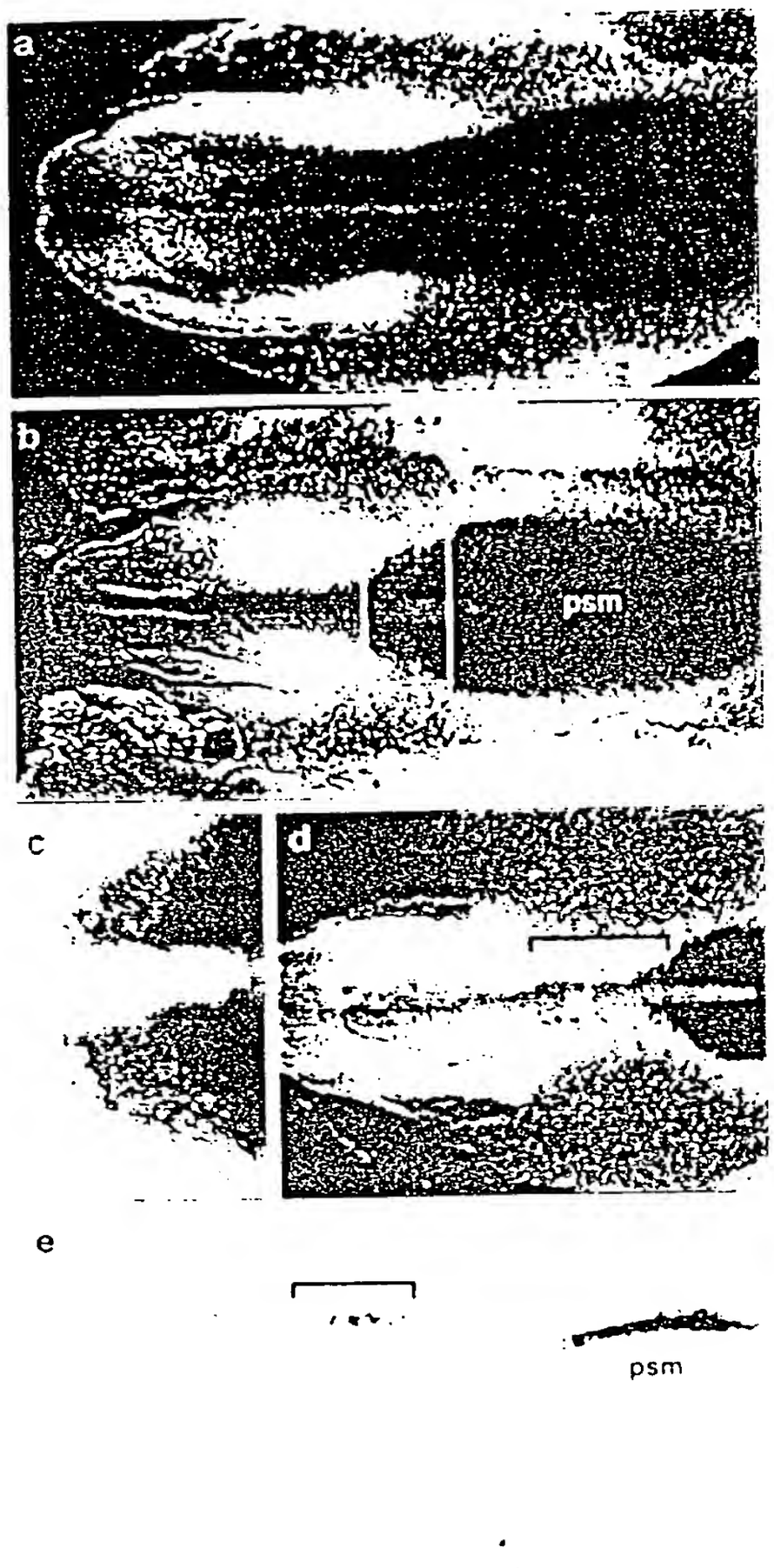

FIG. 5

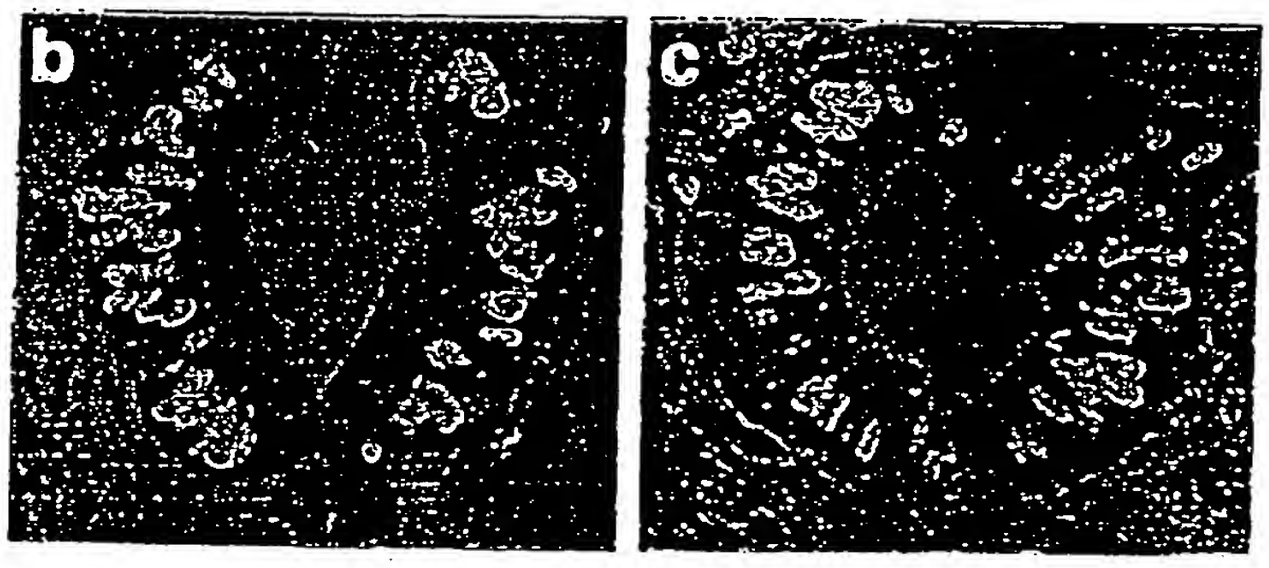

FIG. 6B FIG. 6C

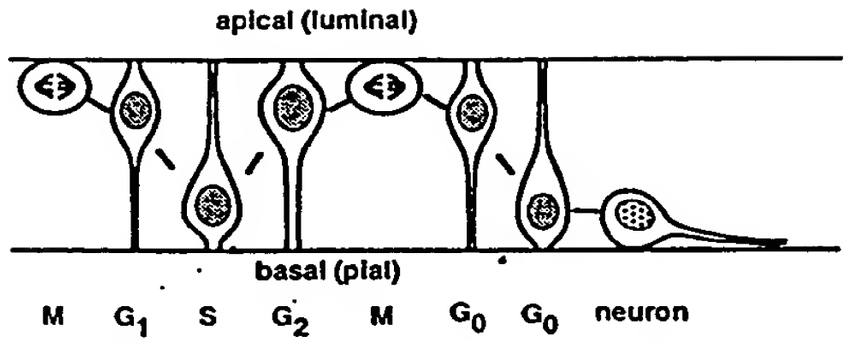

FIG. 6A

```
CTGCAGGAAT TCSMYCGCAT GCTCCCGGCC GCCATGGGCC GTCGGAGCGC GCTAGCCCTT      60
GCCGTGGTCT CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG     120
CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG CGGGGGCTCT     180
GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC TCAAGCACTA CCAGGCCAGC     240
GTGTCACCGG AGCCACCCTG CACCTACGGC AGTGCCGTCA CGCCAGTGCT GGGTGTCGAC     300
TCCTTCAGCC TGCCTGATGG CGCAGGCATC GACCCCGCCT TCAGCAACCC CATCCGATTC     360
CCCTTCGGCT TCACCTGGCC AGGTACCTTC TCTCTGATCA TTGAAGCCCT CCATACAGAC     420
TCTCCCGATG ACCTCGCAAC AGAAAACCCA GAAAGACTCA TCAGCCGCCT GACCACACAG     480
AGGCACCTCA CTGTGGGAGA AGAATGGTCT CAGGACCTTC ACAGTAGCGG CCGCACAGAC     540
CTCCGGTACT CTTACCGGTT TGTGTGTGAC GAGCACTACT ACGGAGAAGG TTGCTCTGTG     600
TTCTGCCGAC CTCGGGATGA CGCCTTTGGC CACTTCACCT GCGGGGACAG AGGGGAGAAG     660
ATGTGCGACC CTGGCTGGAA AGGCCAGTAC TGCACTGACC CAATCTGTCT GCCAGGGTGT     720
GATGACCAAC ATGGATACTG TGACAAACCA GGGGAGTGCA AGTGCAGAGT TGGCTGGCAG     780
GGCCGCTACT GCGATGAGTG CATCCGATAC CCAGGTTGTC TCCATGGCAC CTGCCAGCAA     840
CCCTGGCAGT GTAACTGCCA GGAAGGCTGG GGGGGCCTTT TCTGCAACCA AGACCTGAAC     900
TACTGTACTC ACCATAAGCC GTGCAGGAAT GGAGCCACCT GCACCAACAC GGGCCAGGGG     960
AGCTACACAT GTTCCTGCCG ACCTGGGTAT ACAGGTGCCA ACTGTGAGCT GGAAGTAGAT    1020
GAGTGTGCTC CTAGCCCCTG CAAGAACGGA GCGAGCTGCA CGGACCTTGA GGACAGCTTC    1080
TCTTGCACCT GCCCTCCCGG CTTCTATGGC AAGGTCTGTG AGCTGAGCGC CATGACCTGT    1140
GCAGATGGCC CTTGCTTCAA TGGAGGACGA TGTTCAGATA ACCCTGACGG AGGCTACACC    1200
TGCCATTGCC CCTTGGGCTT CTCTGGCTTC AACTGTGAGA AGAAGATGGA TCTCTGCGGC    1260
TCTTCCCCTT GTTCTAACGG TGCCAAGTGT GTGGACCTCG GCAACTCTTA CCTGTGCCGG    1320
TGCCAGGCTG GCTTCTCCGG GAGGTACTGC GAGGACAATG TGGATGACTG TGCCTCCTCC    1380
CCGTGTGCAA ATGGGGGCAC CTGCCGGGAC AGTGTGAACG ACTTCTCCTG TACCTGCCCA    1440
CCTGGCTACA CGGGCAAGAA CTGCAGCGCC CCTGTCAGCA GGTGTGAGCA TGCACCCTGC    1500
CATAATGGGG CCACCTGCCA CCAGAGGGGC CAGCGCTACA TGTGTGAGTG CGCCCAGGGC    1560
TATGGCGGCC CCAACTGCCA GTTTCTGCTC CCTGAGCCAC CACCAGGGCC CATGGTGGTG    1620
GACCTCAGTG AGAGGCATAT GGAGAGCCAG GGCGGGCCCT TCCCCTGGGT GGCCGTGTGT    1680
GCCGGGGTGG TGCTTGTCCT CCTGCTGCTG CTGGGCTGTG CTGCTGTGGT GGTCTGCGTC    1740
CGGCTGAAGC TACAGAAACA CCAGCCTCCA CCTGAACCCT GTGGGGGAGA GACAGAAACC    1800
ATGAACAACC TAGCCAATTG CCAGCGCGAG AAGGACGTTT CTGTTAGCAT CATTGGGGCT    1860
ACCCAGATCA AGAACACCAA CAAGAAGGCG GACTTTCACG GGGACCATGG AGCCGAGAAG    1920
AGCAGCTTTA AGGTCCGATA CCCCACTGTG GACTATAACC TCGTTCGAGA CCTCAAGGGA    1980
GATGAAGCCA CGGTCAGGGA TACACACAGC AAACGTGACA CCAAGTGCCA GTCACAGAGC    2040
TCTGCAGGAG AAGAGAAGAT CGCCCCAACA CTTAGGGGTG GGGAGATTCC TGACAGAAAA    2100
AGGCCAGAGT CTGTCTACTC TACTTCAAAG GACACCAAGT ACCAGTCGGT GTATGTTCTG    2160
TCTGCAGAAA AGGATGAGTG TGTTATAGCG ACTGAGGTGT AAGATGGAAG CGATGTGGCA    2220
AAATTCCCAT TTCTCTTAAA TAAAATTCCA AGGATATAGC CCCGATGAAT GCTGCTGAGA    2280
GAGGAAGGGA GAGGAAACCC AGGGACTGCT GCTGAGAACC AGGTTCAGGC GAACGTGGTT    2340
CTCTCAGAGT TAGCAGAGGC GCCCGACACT GCCAGCCTAG GCTTTGGCTG CCGCTGGACT    2400
GCCTGCTGGT TGTTCCCATT GCACTATGGA CAGTTGCTTT GAAGAGTATA TATTTAAATG    2460
GACGAGTGAC TTGATTCATA TAGGAAGCAC GCACTGCCCA CACGTCTATC TTGGATTACT    2520
ATGAGCCAGT CTTTCCTTGA ACTAGAAACA CAACTGCCTT TATTGTCCTT TTTGATACTG    2580
AGATGTGTTT TTTTTTTTTC CTAGACGGGA AAAAGAAAAC GTGTGTTATT TTTTTTGGGA    2640
TTTGTAAAAA TATTTTTCAT GATTATGGGA GAGCTCCCAA CGCGTTGGAG GT            2692
```

FIG. 7

```
MGRRSALALA VVSALLCQVW SSGVFELKLQ EFVNKKGLLG NRNCCRGGSG      50
PPCACRTFFR VCLKHYQASV SPEPPCTYGS AVTPVLGVDS FSLPDGAGID     100
PAFSNPIRFP FGFTWPGTFS LIIEALHTDS PDDLATENPE RLISRLTTQR     150
HLTVGEEWSQ DLHSSGRTDL RYSYRFVCDE HYYGEGCSVF CRPRDDAFGH     200
FTCGDRGEKM CDPGWKGQYC TDPICLPGCD DQHGYCDKPG ECKCRVGWQG     250
RYCDECIRYP GCLHGTCQQP WQCNCQEGWG GLFCNQDLNY CTHHKPCRNG     300
ATCTNTGQGS YTCSCRPGYT GANCELEVDE CAPSPCKNGA SCTDLEDSFS     350
CTCPPGFYGK VCELSAMTCA DGPCFNGGRC SDNPDGGYTC HCPLGFSGFN     400
CEKKMDLCGS SPCSNGAKCV DLGNSYLCRC QAGFSGRYCE DNVDDCASSP     450
CANGGTCRDS VNDFSCTCPP GYTGKNCSAP VSRCEHAPCH NGATCHQRGQ     500
RYMCECAQGY GGPNCQFLLP EPPPGPMVVD LSERHMESQG GPFPWVAVCA     550
GVVLVLLLLL GCAAVVVCVR LKLQKHQPPP EPCGGETETM NNLANCQREK     600
DVSVSIIGAT QIKNTNKKAD FHGDHGAEKS SFKVRYPTVD YNLVRDLKGD     650
EATVRDTHSK RDTKCQSQSS AGEEKIAPTL RGGEIPDRKR PESVYSTSKD     700
TKYQSVYVLS AEKDECVIAT EV                                   722
```

FIG. 8

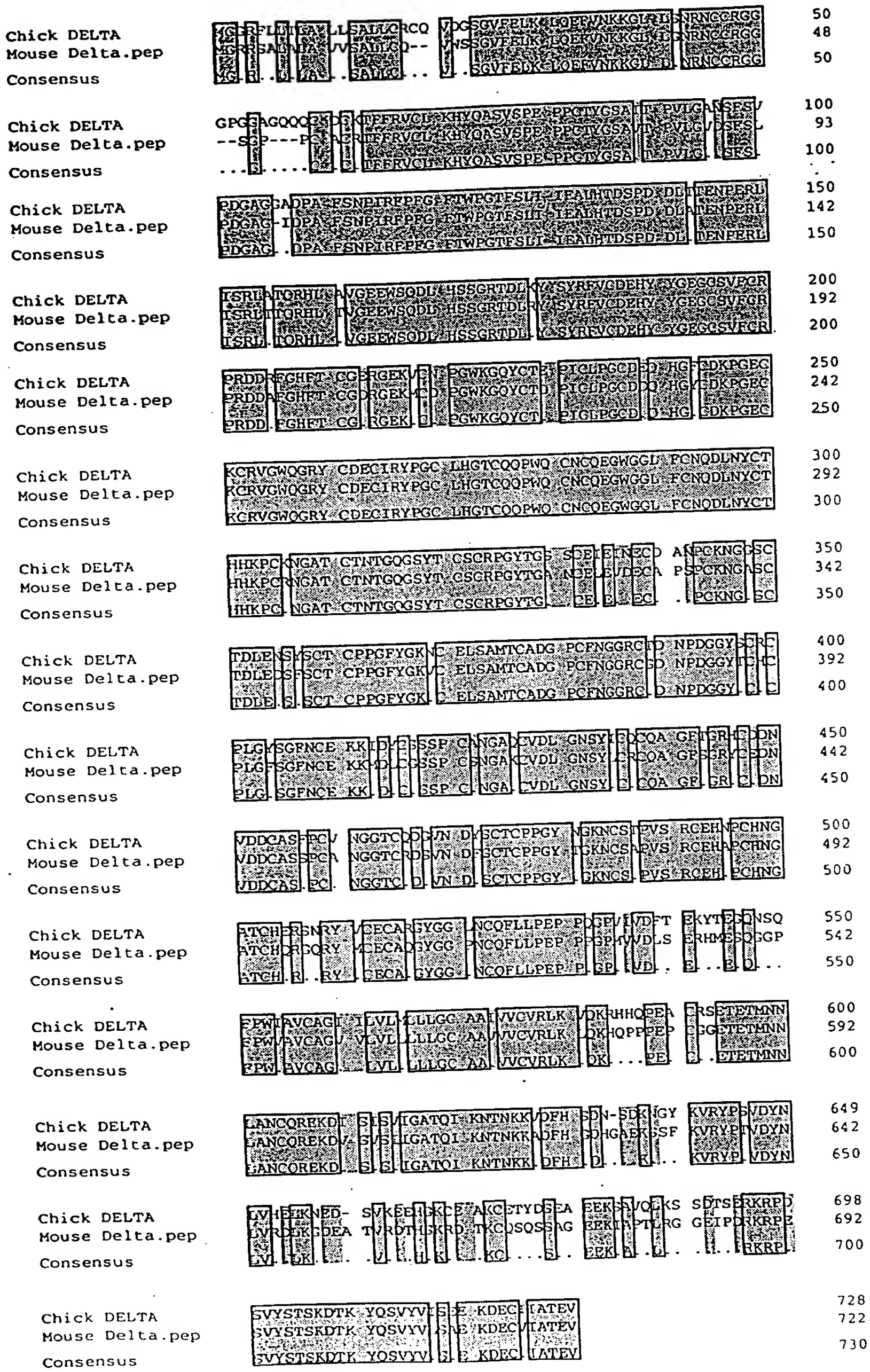

FIG. 9

```
          10          20          30          40          50          60
                       *           *                       *
TACGATGAAY AACCTGGCGA ACTGCCAGCG TGAGAAGGAC ATCTCAGTCA GCATCATCGG
 Y  D  E   X  P  G  E   L  P  A   *  E  G   H  L  S  Q   H  H  R>
  T  M  N   N  L  A   N  C  Q  R   E  K  D   I  S  V   S  I  I  G>
   R  *  X   T  W  R   T  A  S   V  R  R  T   S  Q  S   A  S  S>

          70          80          90          100         110         120
                       *                       *                       *
GGCYACGTCA GATCARGAAC ACCAACAAGA AGGCGGACTT YMCASCGGGG GACCASAGCG
 G  X  V   R  S  X  T   P  T  R   R  R  T   X  X  R  G   T  X  A>
  A  T  S   D  Q  E   H  Q  Q  E   G  G  L   X  X  G  G   P  X  R>
G  X  R  Q   I  X  N   T  N  K   K  A  D  F   X  X  G  D   X  S>

          130         140         150         160         170         180
                       *                       *                       *
TCCGACAAGA ATGGMTTTCA AGGCCCGCTA CCCCAGCGTG GACTATAACT CGTGCAGGAC
 S  D  K   N  G  F  Q   G  P  L   P  Q  R   G  L  *  L   V  Q  D>
  P  T  R   M  X  F   K  A  R  Y   P  S  V   D  Y  N   S  C  R  T>
V  R  Q  E   W  X  S   R  P  A   T  P  A  W   T  I  T   R  A  G>

          190         200         210         220         230         240
                       *                       *                       *
CTCAAGGGTG ACGACACCGC CGTCAGGACG TCGCACAGCA AGCGTGACAC CAAGTGCCAG
 L  K  G   D  D  T  A   V  R  T   S  H  S   K  R  D  T   K  C  Q>
  S  R  V   T  T  P   P  S  G  R   R  T  A   S  V  T   P  S  A  S>
P  Q  G  *   R  H  R   R  Q  D   V  A  Q  Q   A  *  H   Q  V  P>

          250         260         270         280         290         300
                       *                       *                       *
TCCCCAGGCT CCTCAGGGAG GAGAAGGGGA CCCCGACCAC ACTCAGGGGK TGCGTGCTGC
 S  P  G   S  S  G  R   R  R  G   P  R  P   H  S  G  X   A  C  C>
  P  Q  A   P  Q  G   G  E  G  D   P  D  H   T  Q  G   X  R  A  A>
V  P  R  L   L  R  E   E  K  G   T  P  T  T   L  R  G   C  V  L>

          310         320         330         340         350         360
                       *                       *                       *
GGGCCGGGCT CAGGAGGGGG TACCTGGGGG 'GTGTCTTCCT GGAACCACTG CTCCGTTTCT
 G  P  G   S  G  G  G   T  W  G   V  S  S   W  N  H  C   S  V  S>
  G  R  A   Q  E  G   V  P  G  G  .C  L  P   G  T  T   A  P  F  L>
R  A  G  L   R  R  G   Y  L  G   G  V  F  L   E  P  L   L  R  F>
```

FIG. 10

```
          370         380         390         400         410         420
                      *                       *                       *
CTTCCCAAAT GTTCTCATGC ATTCATTGTG GATTTTCTCT ATTTTCCTTT TAGTGGAGAA
 L  P  K    C  S  H  A    F  I  V    D  F  L    Y  F  P  F    S  G  E>
   F  P  N    V  L  M    H  S  L  W    I  F  S    I  F  L    L  V  E  K>
S  S  Q  M    F  S  C    I  H  C    G  F  S  L    F  S  F    *  W  R>

          430         440         450         460         470         480
                      *                       *                       *
GCATCTGAAA GAAAAAGGCC GGACTCGGGC TGTTCAACTT CAAAAGACAC CAAGTACCAG
 A  S  E    R  K  R  P    D  S  G    C  S  T    S  K  D  T    K  Y  Q>
   H  L  K    E  K  G    R  T  R  A    V  Q  L    Q  K  T    P  S  T  S>
S  I  *  K    K  K  A    G  L  G    L  F  N  F    K  R  H    Q  V  P>

          490         500         510         520
                      *                       *
TCGGTGTACG TCATATCCGA GGAGAAGGAC GAGTGCGTCA TCGCA
 S  V  Y    V  I  S  E    E  K  D    E  C  V    I  A>
   R  C  T    S  Y  P    R  R  R  T    S  A  S    S>
V  G  V  R    H  I  R    G  E  G    R  V  R  H    R>
```

FIG. 10 (cont'd)

```
  1 TMNNLANCQREKDISVSIIGATQIXNTNKKADFXXGDXSSDKNGFQKARY 50
    ||||||||||||||||:|:|||||| |||||.||  ::  |||||: |.||
597 TMNNLANCQREKDISISVIGATQIKNTNKKVDFHSDN..SDKNGY.KVRY 643

 51 PSVDYNLVQDLKGDDTAVRTSHSKRDTKCQSPGSSGRRRGPRPHSGXACC 100
    ||||||||::||.:| .|:..|:| :.||:. :|.:  :::
644 PSVDYNLVHELKNED.SVKEEHGKCEAKCETYDSEAEEKSA......... 683

101 GPGSGGGTWGVSSWNHCSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSG 150
                                  |::    |::.||||||||.
684 ............................VQLK....SSDTSERKRPDSV 700

151 CSTSKDTKYQSVYVISEEKDECVIA 175
    :||||||||||||||||||||:||
701 YSTSKDTKYQSVYVISEEKDECIIA 725
```

FIG. 11

```
        10          20          30          40          50          60
    *   *   *   *   *   *   *   *   *   *   *   *
CATTGGGTAC GGGCCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCCGG

        70          80          90          100         110         120
    *   *   *   *   *   *   *   *   *   *   *   *
CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA

        130         140         150         160         170         180
    *   *   *   *   *   *   *   *   *   *   *   *
TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT

        190         200         210         220         230         240
    *   *   *   *   *   *   *   *   *   *   *   *
GACGGTGGGC CAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAGTA

        250         260         270         280         290         300
    *   *   *   *   *   *   *   *   *   *   *   *
CTCCTACCGC TTCGTGTGTC ACCAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTCCCG

        310         320         330         340         350         360
    *   *   *   *   *   *   *   *   *   *   *   *
TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA

        370         380         390         400         410         420
    *   *   *   *   *   *   *   *   *   *   *   *
CCCTGGCTGG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA

        430         440         450         460         470         480
    *   *   *   *   *   *   *   *   *   *   *   *
GCATGGATTT TGTGACAAAC CAGCGGAATG CAAGTGCAGA GTGGGCTGGC AGGGCCGGTA

        490         500         510         520         530         540
    *   *   *   *   *   *   *   *   *   *   *   *
CTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA

        550         560         570         580         590         600
    *   *   *   *   *   *   *   *   *   *   *   *
GTGCAACTGC CAGGAAGGNT GGGGGCCCCT TTTCTGCAAC CAGGACCTGA ACTACTGCAC

        610         620         630         640         650         660
    *   *   *   *   *   *   *   *   *   *   *   *
ACACCATAAG CCCTGCAAGA ATGGAGCCAC CTGCAACAAA CACGGGCCAG GGGGAGCTAC

        670         680         690         700         710         720
    *   *   *   *   *   *   *   *   *   *   *   *
ACTTGGTCTT TGGCCGGNCT GGGGTACANA GGGTGCCACC TGCGAAGCTT GGGGATTGGA

        730         740         750         760         770         780
    *   *   *   *   *   *   *   *   *   *   *   *
CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC

        790         800         810         820         830         840
    *   *   *   *   *   *   *   *   *   *   *   *
AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG

        850         860         870         880         890         900
    *   *   *   *   *   *   *   *   *   *   *   *
ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTCGGTGCT CAGACAGCCC CGATGGAGGG
```

FIG. 12A

```
      910         920         930         940         950         960
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
TACAGCTGCC GCTGCCCCGT GGGCTACTCC GGCTTCAACT GTGAGAAGAA AATTGACTAC

      970         980         990        1000        1010        1020
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
TGCAGCTCTT CACCCTGTTC TAATGGTGCC AAGTGTGTGG ACCTCGGTGA TGCCTACCTG

     1030        1040        1050        1060        1070        1080
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
TGCCGCTGCC AGGCCGGCTT CTCGGGGAGG CACTGTGACG ACAACGTGGA CGACTGCGCC

     1090        1100        1110        1120        1130        1140
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
TCCTCCCCGT GCGCCAACGG GGGCACCTGC CGGGATGGCG TGAACGACTT CTCCTGCACC

     1150        1160        1170        1180        1190        1200
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
TGCCCGCCTG GCTACACGGG CAGGAACTGC AGTGCCCCCG CCAGCACGTG CGAGCACGCA

     1210        1220        1230        1240        1250        1260
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
CCCTGCCACA ATGGGGCCAC CTGCCACGAG AGGGGCCACC GCTATNTGTG CGAGTGTGCC

     1270        1280        1290        1300        1310        1320
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
CGAAGCTACG GGGGTCCCAA CTCCCANTTC CTGCTCCCCC AAACTGCCCC CCCGGCCCCA

     1330        1340        1350        1360        1370        1380
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
CGGTGGTGGA AACTCCCCTA AAAAAACCTA AAAGGGCCGG GGGGGGCCCA TCCCCTTGGT

     1390        1400        1410        1420        1430        1440
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
GGACGTGTGC GCCGGGGTCA TCCTTGTCCT CATGCTGCTC CTGGGCTGTG CCGCTGTGGT

     1450        1460        1470        1480        1490        1500
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
GGTCTGCGTC CGGCTGAGGC TGCAGAAGCA CCGGCCCCCA GCCGACCCCT GNCGGGGGGA

     1510        1520        1530        1540        1550        1560
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
GACGGAGACC ATGAACAACC TGGNCAACTG CCAGCGTGAG AAGGACATCT CAGTCAGCAT

     1570        1580        1590        1600        1610        1620
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
CATCGGGGNC ACGCAGATCA AGAACACCAA CAAGAAGGCG GACTTCCACG GGGACCACAG

     1630        1640        1650        1660        1670        1680
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
NGCCGACAAG AATGGCTTCA AGGCCCGCTA CCCAGNGGTG GACTATAACC TCGTGCAGGA

     1690        1700        1710        1720        1730        1740
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
CCTCAAGGGT GACGACACCG CCGTCAGCOA CGCGCACAGC AAGCGTGACA CCAAGTGNCA

     1750        1760        1770        1780        1790        1800
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
GCCCCAGGGC TCCTCAGGGG AGGACAAGGG GACCCCCGAC CCACACTCAG GGGGTGGAGG

     1810        1820        1830        1840        1850        1860
    *   *     *   *     *   *
```

FIG. 12A (cont'd)

```
AAGCATCTTG AAAGAAAAAG GCCGGACTTC GGGCTTGTTC AACTTTCAAA AGACAANCAA
        1870       1880       1890       1900       1910       1920
 *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
NGTACAAGTC GGTGTNCGTC ATTTCCGNAG GAGGAAGGNT GACTGCGTCA TAGGAANTTG
        1930       1940       1950       1960       1970       1980
 *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
AGGTNGTTAAA NTGGNAGTTG ANNTTGCAAA GNNNTCCCCG GATTCCGNTT TCAAAGTTTT
T
```

FIG. 12A (cont'd)

```
          10         20         30         40         50         60
        *  *       *  *       *  *       *  *       *  *       *  *   a.a. no.
CATTGGGTAC GGGCCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCCGG
 H  W  V   R  A  P  L   E  V  D   G  I  D   K  L  D  I   E  F  R>   20
  I  G  Y   G  P  P  S   R  S  T   V  S  I   S  L  I  S   N  S [G>]  20
   L  G  T   G  P  P  R   G  R  R   Y  R  *   A  *  Y  R   I  P>   19

          70         80         90        100        110        120
        *  *       *  *       *  *       *  *       *  *       *  *
CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA
 L  H  L   A  G  H  L   L  S  D   Y  *  S   S  P  H  R   F  S  *>   40
  [F  T  W   P  G  T  F   S  L  I   I  E  A   L  H  T  D   S  P  D>]  40
A  S  P  G   R  A  P  S   L  *  L   L  K  I   S  T  Q  I   L  L  L>   39

         130        140        150        160        170        180
        *  *       *  *       *  *       *  *       *  *       *  *
TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT
 *  P  R   N  R  K  P   R  K  T   H  Q  P   P  G  H  P   E  A  P>   60
 [D  L  A   T  E  N  P   E  R  L   I  S  R   L  A  T  Q   R  H  L>]  60
M  T  S  Q   Q  K  T  Q   K  D  S   S  A  A   W  P  P  R   -  G  T>   59

         190        200        210        220        230        240
        *  *       *  *       *  *       *  *       *  *       *  *
GACGGTGGGC GAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAGTA
 D  G  G   R  G  V  V   P  G  P   A  Q  Q   R  P  H  G   P  Q  V>   80
 [T  V  G   E  E  W  S   Q  D  L   H  S  S   G  R  T  D   L  K  Y>]  80
*  R  W   A  R  S  G   P  R  T   C  T  A   A  A  A  R   T  S  S>   79

         250        260        270        280        290        300
        *  *       *  *       *  *       *  *       *  *       *  *
CTCCTACCGC TTCGTGTGTG ACGAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTGCCG
 L  L  P   L  R  V  *   R  T  L   L  R  R   G  L  L  R   F  L  P>   100
 [S  Y  R   F  V  C  D   E  H  Y   Y  G  E   G  C  S  V   F  C  R>]  100
T  P  T   A  S  C  V   T  N  T   T  T  E   R  A  A  P   F  S  A>   99

         310        320        330        340        350        360
        *  *       *  *       *  *       *  *       *  *       *  *
TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA
 S  P  G   R  C  L  R   P  L  H   L  W  G   A  W  G  E   S  V  Q>   120
 [P  R  D   D  A  F  G   H  F  T   C  G  E   R  G  E  K   V  C  N>]  120
V  P  G   T  M  P  S   A  T  S   P  V  C   S  V  G  R   K  C  A>   119

         370        380        390        400        410        420
        *  *       *  *       *  *       *  *       *  *       *  *
CCCTGGCTGG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA
 P  W  L   E  R  A  L   L  H  R   A  D  L   P  A  W  M   *  *  A>   140
 [P  G  W   K  G  P  Y   C  T  E   P  I  C   L  P  G  C   D  E  Q>]  140
T  L  A   G  K  G  P   T  A  Q   S  R  S   A  C  L  D   V  M  S>   139

         430        440        450        460        470        480
        *  *       *  *       *  *       *  *       *  *       *  *
GCATGGATTT TGTGACAAAC CAGCCCAATG CAAGTGCAGA GTGGGCTGGC AGGGCCGGTA
 A  W  I   L  *  Q  T   R  G  M   Q  V  Q   S  G  L  A   G  P  V>   160
 [H  G  F   C  D  K  P   G  E  C   K  C  R   V  G  W  Q   G  R  Y>]  160
S  M  D   F  V  T  N   Q  G  N   A  S  A   E  W  A  G   R  A  G>   159

         490        500        510        520        530        540
        *  *       *  *       *  *       *  *       *  *       *  *
CTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA
 L  *  R   V  Y  P  L   S  R  L   S  P  W   H  L  P  A   A  L  A>   180
```

FIG. 12B

```
                                                                    C  D  E  C  I  R  Y  P  G  C  L  H  G  T  C  Q  Q  P  W  Q>  180
                                                                 T  V  T  S  V  S  A  I  Q  A  V  S  M  A  P  A  S  S  P  Q>  179

                  550        560        570        580        590        600
                  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
GTGCAACTGC CAGGAAGGNT GGGGGGGCCT TTCTGCAAC CAGGACCTGA ACTACTGCAC
 V  Q  L  P  G  R  X  G  G  P  F  L  Q  P  G  P  E  L  L  H>  200
 C  N  C  Q  E  G  W  G  G  L  F  C  N  Q  D  L  N  Y  C  T>  200
S  A  T  A  R  K  X  G  G  A  F  S  A  T  R  T  *  T  T  A>  199

                  610        620        630        640        650        660
                  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
ACACCATAAG CCCTGCAAGA ATCGAGCCAC CTGCAACAAA CACGGCCCAG GGGGAGCTAC
 T  P  *  A  L  Q  E  W  S  H  L  Q  Q  T  R  A  R  G  S  Y>  220
 H  H  K  P  C  K  N  G  A  T  C  N  K  H  G  P  G  C  A  T>  220
H  T  I  S  P  A  R  M  E  P  P  A  T  N  T  G  Q  G  E  L>  219

                  670        680        690        700        710        720
                  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
ACTTGGTCTT TGGCCGGNCT GGGGTACANA GGGTGCCACC TGCGAAGCTT GGGGATTGGA
 T  W  S  L  A  G  L  G  Y  X  G  C  H  L  R  S  L  G  I  G>  240
 L  G  L  W  P  X  W  G  T  X  G  A  T  C  E  A  W  G  L  D>  240
H  L  V  F  G  R  X  C  V  X  R  V  P  P  A  K  L  G  D  W>  239

                  730        740        750        760        770        780
                  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC
 R  V  V  D  P  S  P  W  *  E  R  R  E  L  D  G  S  S  E  N>  260
 E  L  L  T  P  A  L  G  K  N  G  G  S  L  T  D  L  R  R  T>  260
T  S  C  *  P  Q  P  L  V  R  T  E  Q  A  *  R  I  F  G  E>  259

                  790        800        810        820        830        840
                  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG
 S  Y  S  C  T  C  P  P  G  F  Y  G  K  I  C  E  L  S  A  M>  280
 A  T  P  V  P  A  H  P  A  S  T  A  K  S  V  N  *  V  P  *>  280
Q  L  L  L  Y  L  P  T  R  L  L  R  Q  N  L  *  I  E  C  H>  279

                  850        860        870        880        890        900
                  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTCGGTGCT CACACAGCCC CGATGGAGGG
 T  C  A  D  G  P  C  F  N  G  G  R  C  S  D  S  P  D  G  G>  300
 P  V  R  T  A  L  A  L  T  G  V  G  A  Q  T  A  P  M  E  G>  300
D  L  C  G  R  P  L  L  *  R  G  S  V  L  R  Q  P  R  W  R>  299

                  910        920        930        940        950        960
                  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
TACAGCTGCC GCTGCCCCGT GGGCTACTCC GCCTTCAACT GTGAGAAGAA AATTGACTAC
 Y  S  C  R  C  P  V  G  Y  S  G  F  N  C  E  K  K  I  D  Y>  320
 T  A  A  A  A  P  W  A  T  P  A  S  T  V  R  R  K  L  T  T>  320
V  Q  L  P  L  P  R  G  L  L  R  L  Q  L  *  E  E  N  *  L>  319

                  970        980        990        1000       1010       1020
                  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
TGCAGCTCTT CACCCTGTTC TAATGGTGCC AAGTCTGTGG ACCTCGGTGA TGCCTACCTG
 C  S  S  S  P  C  S  N  G  A  K  C  V  D  L  G  D  A  Y  L>  340
 A  A  L  H  P  V  L  M  V  P  S  V  W  T  S  V  M  P  T  C>  340
L  Q  L  F  T  L  F  *  W  C  Q  V  C  G  P  R  *  C  L  P>  339

                  1030       1040       1050       1060       1070       1080
                  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
TGCCGCTGCC AGGCCGGCTT CTCGCCGAGG CACTGTGACG ACAACGTGGA CGACTGCGCC
```

FIG. 12B (cont'd)

```
C R C  Q A G F  S G R  H C D  D N V D  D C  A>  360
  A A A  R P A  S R G  G T V  T T W  T T  A P>  360
V P L P  G R L  L G E  A L *  R Q R  G R  L R>  359

      1090      1100      1110      1120      1130      1140
    *   *   *   *   *   *   *   *   *   *   *   *
TCCTCCCCGT GCGCCAACGG GGGCACCTGC CGGGATGGCG TGAACGACTT CTCCTGCACC
S S P  C A N G  G T C  R D G  V N D  F S  C T>  380
  P P R  A P T  G A P  A G M  A * T  T S  P A  P>  380
L L P V  R Q R  G H L  P G W  R E R  L L  L H>  379

      1150      1160      1170      1180      1190      1200
    *   *   *   *   *   *   *   *   *   *   *   *
TGCCCGCCTG GCTACACGGG CAGGAACTGC AGTGCCCCCG CCAGCAGGTG CGAGCACGCA
C P P  G Y T  G R N  C S A  P A S  R C  E H  A>  400
  A R L  A T R  A G T  A V P  P P A  G A  S T  H>  400
L P A W  L H G  Q E L  Q C P  R Q Q  V R  A R>  399

      1210      1220      1230      1240      1250      1260
    *   *   *   *   *   *   *   *   *   *   *   *
CCCTGCCACA ATGGGGCCAC CTGCCACGAG AGGGGCCACC GCTATNTGTG CGAGTGTGCC
P C H  N G A  T C H  E R G  H R Y  X  C E C  A>  420
  P A T  M G P  P A T  R G A  T A I  C A S  V P>  420
T L P Q  W G H  L P R  E G P  P L  F V R  V C>  419

      1270      1280      1290      1300      1310      1320
    *   *   *   *   *   *   *   *   *   *   *   *
CGAAGCTACG GGGGTCCCAA CTGCCANTTC CTGCTCCCCG AAACTGCCCC CCCGGCCCCA
R S Y  G G P  N C  X  F L L  P E  T A P  P A P>  440
  E A T  G V P  T A X  S C S  P K L  P P R  P H>  440
P K L R  G S Q  L P X  P A P  R N C  P P G  P>  439

      1330      1340      1350      1360      1370      1380
    *   *   *   *   *   *   *   *   *   *   *   *
CGGTGGTGGA AACTCCCCTA AAAAAACCTA AAAGGGCCGG GGGGGGCCCA TCCCCTTGGT
R W W  K L P *  K N L  K G P  G G A  H P L  G>  460
  G G G  N S P  K K T *  K G R  G G P  I P L  V>  460
T V V  E T P  L K K  P K R  A G G  G P S  P W>  459

      1390      1400      1410      1420      1430      1440
    *   *   *   *   *   *   *   *   *   *   *   *
GGACGTGTGC GCCGGGGTCA TCCTTGTCCT CATGCTGCTG CTGGGCTGTC CCGCTGTGGT
G R V  R R G H  P C P  H A A  A G L  C R C  G>  480
  D V C  A G V  I L V  L M L  L L  G C  A A  V V>  480
W T C A  P G S  S L S  S C C  C W  A V  P L  W>  479

      1450      1460      1470      1480      1490      1500
    *   *   *   *   *   *   *   *   *   *   *   *
GGTCTGCGTC CGGCTGAGGC TGCAGAAGCA CCGGCCCCCA GCCGACCCCT GNCGGGGGGA
G L R  P A E  A A E  A P A  P S  R P  L X  G G>  500
  V C V  R L R  L Q K  H R P  P A  D P  X R  G E>  500
W S A S  G * G  C R S  T G P  Q P  T P  X G  G>  499

      1510      1520      1530      1540      1550      1560
    *   *   *   *   *   *   *   *   *   *   *   *
GACGGAGACC ATGAACAACC TGGNCAACTG CCAGCGTGAG AAGGACATCT CAGTCAGCAT
D G D  H E Q  P G  Q L  P A *  E G  H L  S Q  H>  520
  T E T  M N N  L X  N C  Q R  E K  D I  S V  S I>  520
R R R P  * T T  W X  T A  S V  R R  T S  Q S  A>  519

      1570      1580      1590      1600      1610      1620
    *   *   *   *   *   *   *   *   *   *   *   *
```

FIG. 12B (cont'd)

```
CATCGGGGNC ACGCAGATCA AGAACACCAA CAAGAAGGCG GACTTCCACG GGGACCACAG
 H R G   H A D Q E H Q Q E G G L P R G P Q>  540
 I G X   T Q I K N T N K K A D F H G D H X>  540
S S G X  R R S R T P T R R R T S T G T T>    539

      1630      1640      1650      1660      1670      1680
 *    *    *    *    *    *    *    *    *    *    *    *
NGCCGACAAG AATGGCTTCA AGGCCCGCTA CCCACNGGTG GACTATAACC TCGTGCAGGA
 X R Q E W L Q G P L P X G G L * P R A G>  560
 A D K N G F K A R Y P X V D Y N L V Q D>  560
X P T R M A S R P A T Q X W T I T S C R>  559

      1690      1700      1710      1720      1730      1740
 *    *    *    *    *    *    *    *    *    *    *    *
CCTCAAGGGT GACGACACCG CCGTCAGGGA CGCGCACAGC AAGCGTGACA CCAAGTGNCA
 P Q G * R H R R Q G R A Q Q A * H Q V X>  580
 L K G D D T A V R D A H S K R D T K X Q>  580
T S R V T T P P S G T R T A S V T P S X>  579

      1750      1760      1770      1780      1790      1800
 *    *    *    *    *    *    *    *    *    *    *    *
GCCCCAGGGC TCCTCAGGGG AGGAGAAGGG GACCCCCGAC CCACACTCAG GGGGTGGAGG
 A P G L L R G G E G D P R P T L R G W R>  600
 P Q G S S G E E K G T P D P H S G G G G>  600
S P R A P Q G R R R G P P T H T Q G V R>  599

      1810      1820      1830      1840      1850      1860
 *    *    *    *    *    *    *    *    *    *    *    *
AAGCATCTTG AAAGAAAAAG GCCGGACTTC GGGCTTGTTC AACTTTCAAA AGACAANCAA
 K H L E R K R P D F G L V Q L S K D X Q>  620
 S I L K E K G R T S G L F N F Q K T X X>  620
E A S * K K K A G L R A C S T F K R Q X>  619

      1870      1880      1890      1900      1910      1920
 *    *    *    *    *    *    *    *    *    *    *    *
NGTACAAGTC GGTGTNCGTC ATTTCCGNAG GAGGAAGGNT GACTGCGTCA TAGGAANTTG
 X T S R C X S F P X E E G * L R H R X L>  640
 V Q V G V R H F R R R K X D C V T G X *>  640
X Y K S V X V I S X G G R X T A S * E X>  639

      1930      1940      1950      1960      1970      1980
 *    *    *    *    *    *    *    *    *    *    *    *
AGGTNGTAAA NTGGNAGTTG ANNTTGGAAA GNNNTCCCCC GATTCCCNTT TCAAAGTTTT
 R X * X G S * X W K X X P G F R F Q S F>  660
 G X K X X V X X G K X S P D S X F K V F>  660
E V V X W X L X L E X X P R I P X S K F>  659

T
```

FIG. 12B (cont'd)

Mouse Delta vs Partial Human Delta

```
Mouse Delta DNA  GTCCAGCGGT ACCATGGGCC GTCGGAGCGC GCTACCCCTT GCCGTGGTCT  50
Human Delta      ---------- ---------- ---------- ---------- ----------
Consensus        GTCCAGCCGT ACCATGGGCC GTCGGAGCGC GCTAGCCCTT GCCGTGGTCT  50

Mouse Delta DNA  CTGCCCTGCT GTGCCAGGTC TGGACCTCCG GCGTATTTGA GCTGAAGCTG  100
Human Delta      ---------- ---------- ---------- ---------- ----------
Consensus        CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG  100

Mouse Delta DNA  CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG  150
Human Delta      ---------- ---------- ---------- ---------- ----------
Consensus        CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG  150

Mouse Delta DNA  CGGGGGCTCT GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC  200
Human Delta      ---------- ---------- ---------- ---------- ----------
Consensus        CGGGGGCTCT GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC  200

Mouse Delta DNA  TCAAGCACTA CCAGGCCAGC GTGTCACCGG AGCCACCCTG CACCTACGGC  250
Human Delta      ---------- ---------- ---------- ---------- ----------
Consensus        TCAAGCACTA CCAGGCCACC GTGTCACCGG AGCCACCCTG CACCTACGGC  250

Mouse Delta DNA  AGTGCTGTCA CGCCAGTGCT GGGTGTCGAC TCCTTCAGCC TGCCTGATGG  300
Human Delta      ---------- ---------- ---------- ---------- -----CATGG    5
Consensus        AGTGCTGTCA CGCCAGTGCT CGGTGTCGAC TCCTTCAGCC TGCCTSATGG  300

Mouse Delta DNA  CGGAAGCATC GACCCC--CG CGTTCAGCAA CCCCA--TCC GATCTC-CCC  343
Human Delta      GGTAGGGGCC CGCCTCGAGG TCGACGGTAT CGATAAGCTT GATATCGAAT   55
Consensus        SGMASGSRYC SMCCYCGAGG MCKWCFGMAW CSMYAAGYYY GATMTCGMMY  350

Mouse Delta DNA  TTCGGCTTCA CCTGGCCAGG TACCTTCTCT CTGATCATTG AAGCCTCTCA  393
Human Delta      TTCGGCTTCA CCTGGCCAGG TACCTTCTCT CTGATCATTG AAGCCTCTCA  105
Consensus        TTCGGCTTCA CCTGGCCAGG TACCTTCTCT CTGATCATTG AAGCCTCTCA  400

Mouse Delta DNA  TACAGACTCT CCCGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  443
Human Delta      CACAGACTCT CCTGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  155
Consensus        YACAGACTCT CCYGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  450

Mouse Delta DNA  GCCGCCTGAC CACACAGAGG CACCTCACTG TGGGCGAAGA CTGGTCTCAG  493
Human Delta      GCCGCCTGCC CACCCAGAGG CACCTGACGG TGGGCGAGGA CTGGTCCCAG  205
Consensus        GCCGCCTGRC CACMCAGAGG CACCTSACKG TGGGCGARGA CTGGTCMCAG  500

Mouse Delta DNA  GACCTTCACA GTAGCGCCCG CACAGACCTC CGGTACTCTT ACCGCTTTGT  543
Human Delta      GACCTGCACA GCAGCGGCCG CACGGACCTC AAGTACTCCT ACCGCTTCGT  255
Consensus        GACCTKCACA GMAGCGGCCG CACKGACCTC MKGTACTCYT ACCGCTTYGT  550

Mouse Delta DNA  GTGTGACGAG CACTACTACG GAGAAGGCTG CTCTGTCTTC TGCCGACCTC  593
Human Delta      GTGTGACCAA CACTACTACG GAGAGGGCTG CTCCGTCTTC TGCCGCCCCC  305
Consensus        GTGTGACGAR CACTACTACG GAGARGGCTG CTCMGTCTTC TGCCGACCMC  600

Mouse Delta DNA  GGGATGAGGC CTTTGGCCAC TTCACCTGCG GGGACAGAGG GGAGAAGATG  643
Human Delta      GGGACGATGC CTTCGGCCAC TTCACCTGTG GGGAGCGGTGG GGAGAAACTG  355
Consensus        GGGAMGAKGC CTTYGGCCAC TTCACCTGMG GGGASMGAGG GGAGAARRTG  650
```

FIG. 13

Mouse Delta vs Partial Human Delta

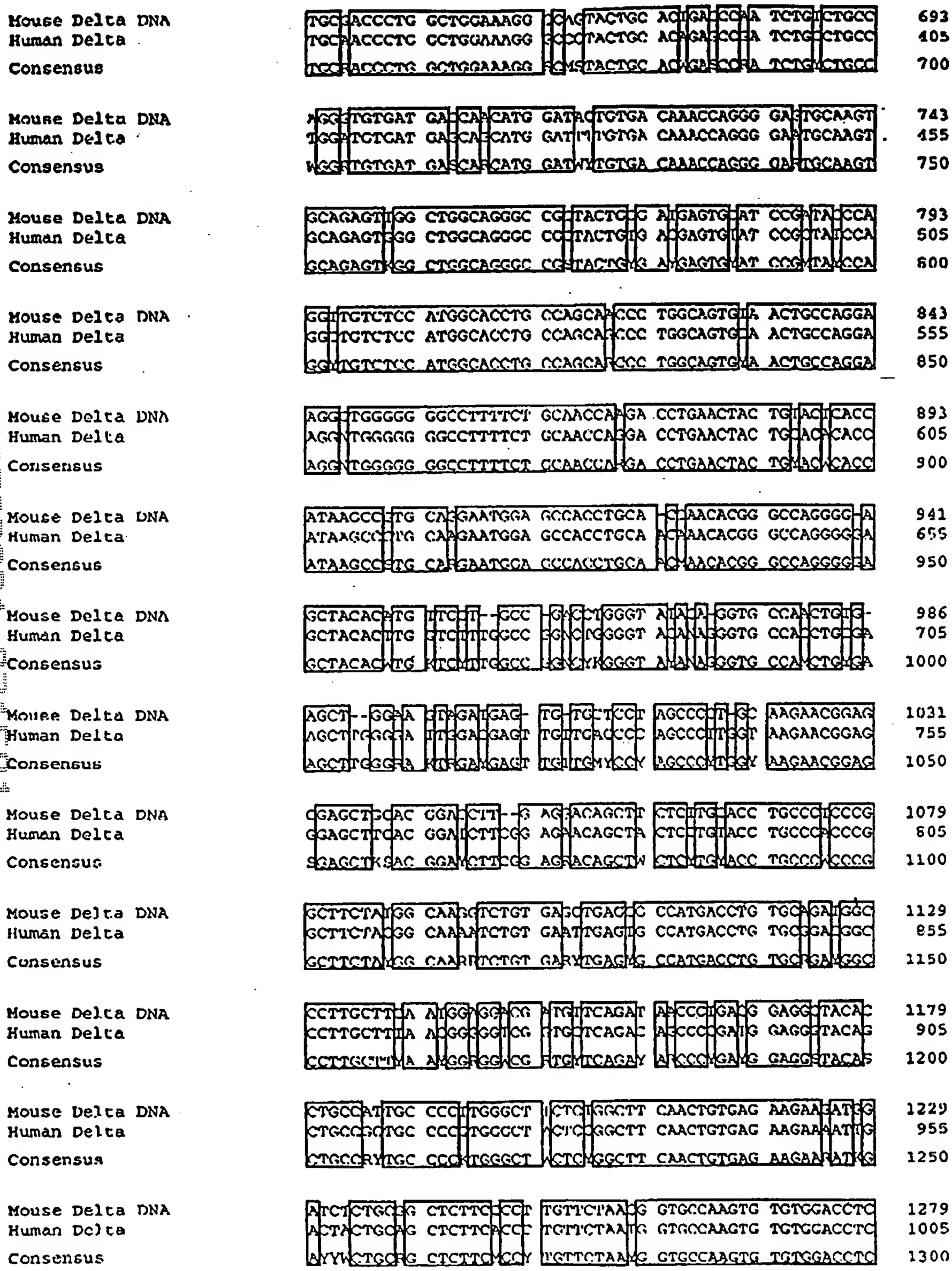

FIG. 13 (cont'd)

Mouse Delta vs Partial Human Delta

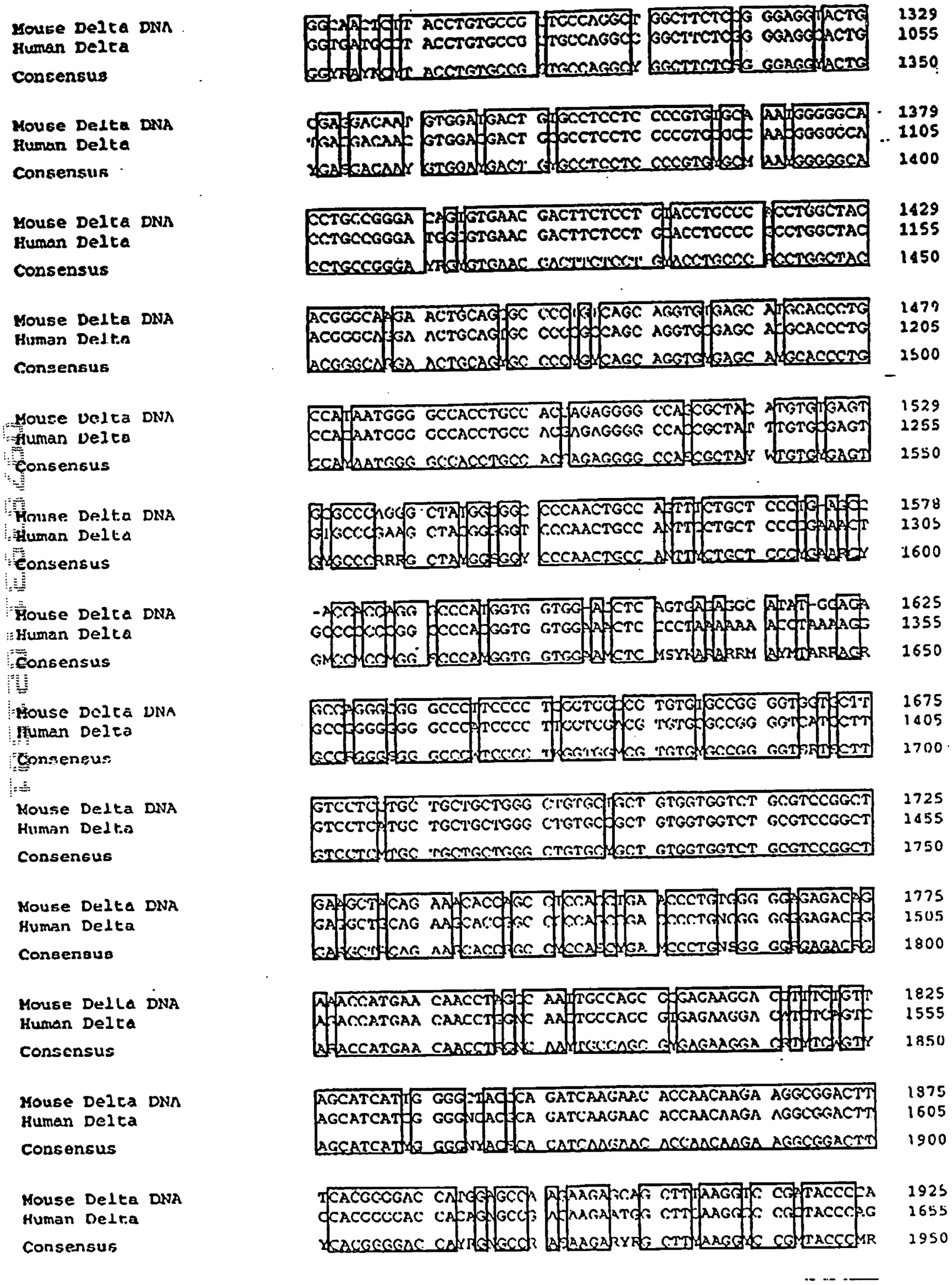

FIG. 13 (cont'd)

Mouse Delta vs Partial Human Delta

```
Mouse Delta DNA  CTGTGGACTA TAACCTCGTT CGAGACCTCA AGGGAGATGA AGCCACGGTC  1975
Human Delta      NGGTGGACTA TAACCTCGTG CAGGACCTCA AGGGTGACGA CACCCCGTC  1705
Consensus        NKGTGGACTA TAACCTCGTK CRRGACCTCA AGGGAGAMGA MRCCRCSGTC  2000

Mouse Delta DNA  AGGGATACAC ACAGCAAACG TGACACCAAG TGCCAGTCAC AGAGCTCTGC  2025
Human Delta      AGGGACCCGC ACAGCAAGCG TCACACCAAG TGTCAGCCCC AGTGCTCCTC  1755
Consensus        AGGGAYYCRC ACAGCAARCG TGACACCAAG TGYCAGMCMC AGWGCTCYKC  2050

Mouse Delta DNA  AGGAGAAGAG AA--GATCG CC--CCAACA CTTA-GGGGT GC-GG-AGAT  2067
Human Delta      ACGGGAGGAG AAGGGGACCC CCGACCCACA CTCAGGGGGT GGAGGAAGCA  1805
Consensus        AGGRGARGAG AAGGGGAMCS CCGACCMACA CTMAGGGGGT GGRGGRAGMW  2100

Mouse Delta DNA  TCTTGAAAGA AAAAGGCCAG AGTCT--GTC TACTCTAC-T TCAAAGGAC-  2113
Human Delta      TCTTGAAAGA AAAAGGCCGG ACTTCGGGCT TGTTCTACTT TCAAAAGACA  1855
Consensus        TCYTGAMAGA AAAAGGCCRG AKTYYGGGYY TRYTCTACTT TCAAARGACA  2150

Mouse Delta DNA  -ACCAAGTAC CAGTCGGTGT ATGTTCTGTC TGCAGAA--A AGGATGACTG  2160
Human Delta      ANCTAAGTAC AAGTCGGTGT NCGTCATTTC CGNAGGAGCA AGGNTGACTG  1905
Consensus        ANCMAMGTAC MAGTCGGTGT NYGTYMTKTC MGNACRAGCA AGGNTGASTG  2200

Mouse Delta DNA  TGTTATA-GC GACTGAGCT- GTAAGATGGA AGCGATGTGG CAAAATTCCC  2208
Human Delta      CGTCATAGGA ANTTGAGGTN GTAAANTGGN AG--T-TG- --ANNTT---  1945
Consensus        YGTMATAGGM RNYTGAGGTN GTAARNTGGN AGCGATGTGG CAANNTTCCC  2250

Mouse Delta DNA  ATTTCTCTCA AATAAAATTC CAAGGATATA GCCCCGATGA ATGCTGCTGA  2258
Human Delta      ----CCCCGA AAGNNN-TTC CCCGGAT--- --TCCGNT-- ----TTC---  1972
Consensus        ATTTCTCKSA AAKNNNATTC CMMCGATATA GCYCCGNTGA ATGCTKCTGA  2300

Mouse Delta DNA  GAGACGAAGG GAGAGCAAAC CCACGGACTG CTGCTGAGAA CCAGGTTCAG  2308
Human Delta      -- -------- --------AAA- --------TC TTTTT----- ----------  1981
Consensus        GAGAGGAAGG GAGAGCAAAC CCAGGGACTG MTKYTCAGAA CCAGGTTCAG  2350

Mouse Delta DNA  GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTGCCAGCCT  2358
Human Delta      -- ----- - -- ---- -- - -------- ---------- ----------  1981
Consensus        GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTGCCAGCCT  2400

Mouse Delta DNA  AGGCTTTGGC TGCCGCTGGA CTGCCTGCTG GTTGTTCCCA TTGCACTATG  2408
Human Delta      -- ---- -- ---------- ----- --- ---------- ----------  1981
Consensus        AGGCTTTGGC TGCCGCTGGA CTGCCTGCTG GTTGTTCCCA TTGCACTATG  2450

Mouse Delta DNA  GACAGTTGCT TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA  2458
Human Delta      ---------- --------- ---------- ---------- ----------  1981
Consensus        GACAGTTGCT TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA  2500

Mouse Delta DNA  TATAGGAAGC ACGCACTGCC CACACGTCTA TCTTGGATTA CTATGAGCCA  2508
Human Delta      - -------  ---- ---- ----  ---- --- ------ ----------  1981
Consensus        TATAGGAAGC ACGCACTGCC CACACGTCTA TCTTGGATTA CTATGAGCCA  2550

Mouse Delta DNA  GTCTTTCCTT GAACTAGAAA CACAACTGCC TTTATTGTCC TTTTTGATAC  2558
Human Delta      ----- ---- ---- ----- ---- ----- ---------- ----------  1981
Consensus        GTCTTTCCTT GAACTAGAAA CACAACTGCC TTTATTGTCC TTTTTGATAC  2600
```

FIG. 13 (cont'd)

Mouse Delta vs Partial Human Delta

```
Mouse Delta DNA   TGAGATGTGT TTTTTTTTT CCTAGACGGG AAAAAGAAAA CCTGTGTTAT   2608
Human Delta       ---------- --------- ---------- ---------- ----------   1981
Consensus         TGAGATGTGT TTTTTTTTT CCTAGACGGG AAAAAGAAAA CGTGTGTTAT   2650

Mouse Delta DNA   TTTTTTGGGA TTTGTAAAAA TATTTTTCAT GATATCTGTA AAGCTTGAGT   2658
Human Delta       ---------- ------ -- ---------- ---------- ----------   1961
Consensus         TTTTTTGGGA TTTGTAAAAA TATTTTTCAT GATATCTGTA AAGCTTGAGT   2700

Mouse Delta DNA   ATTTTGTGAC GTTCATTTTT TTATAATTTA AATTTTGGTA AATATGTACA   2708
Human Delta       ---------- ----- ---- ---------- ---------- ----------   1981
Consensus         ATTTTGTGAC GTTCATTTTT TTATAATTTA AATTTTGGTA AATATGTACA   2750

Mouse Delta DNA   AAGGCACTTC GGGTCTATGT GACTATATTT TTTTGTATAT AAATGTATTT   2758
Human Delta       ---------- ----- --- --------- --------- ----------   1981
Consensus         AAGGCACTTC GGGTCTATGT GACTATATTT TTTTGTATAT AAATGTATTT   2800

Mouse Delta DNA   ATGCAATATT GTGCAAATGT TATTTGAGTT TTTTACTGTT TTGTTAATGA   2008
Human Delta       ---------- -- ------ -- -- ------- ------- ----------   1981
Consensus         ATGGAATATT GTGCAAATGT TATTTGAGTT TTTTACTGTT TTGTTAATGA   2850

Mouse Delta DNA   AGAAATTCAT TTTAAAAATA TTTTTCCAAA ATAAATATAA TGAACTACA    2857
Human Delta       ---------- ---------- --------- ---------- ---------    1981
Consensus         AGAAATTCAT TTTAAAAATA TTTTTCCAAA ATAAATATAA TGAACTACA    2899
```

FIG. 13 (cont'd)

```
G F T W P G T F S L I I E A L H T D S P D>  21
D L A T E N P E R L I S R L A T Q R H L>  41
T V G E E W S Q D L H S S G R T D L K Y>  61
S Y R F V C D E H Y Y G E G C S V F C R>  81
P R D D A F G H F T C G E R G E K V C N>  101
P G W K G P Y C T E P I C L P G C D E Q>  121
H G F C D K P G E C K C R V G W Q G R Y>  141
C D E C I R Y P G C L H G T C Q Q P W Q>  161
C N C Q E G W G G L F C N Q D L N Y C T>  181
H H K P C K N G A T C * T N T G Q G *  198
S Y T * P S R * K N G G S L T D L *  213
E N S Y S C T C P P G F Y G K I C E L S A M>  235
T C A D G P G F N G G R C S D S P D G G>  255
Y S C R C P V G Y S G F N C E K K I D Y>  275
C S S S P C S N G A K C V D L G D A Y L>  295
C R C Q A G F S G R H C D D N V D D C A>  315
S S P C A N G G T C R D G V N D F S C T>  335
C P P G Y T G R N C S A P A S R C E H A>  355
P C H N G A T C H F R G H R Y * C E C A>  374
R S Y G G P N C * F L L P E * P P G P *  391
V V * L L L G C A A V V V C V R L R L Q K H>  412
R P P A D P * R G E T E T M N N L *  428
N C Q R E K D I S V S I I G * T Q I K N T N>  449
K K A D F H G D H * A D K N G F K A R Y P *  469
V D Y N L V Q D L K G D D T A V R D A H S K R D T K *  495
Q P Q G S S G E E K G T P * P T L R * G G *  514
I * K K R P * S * S T * S K D * T *  526
C V I * E V *  531
```

FIG. 14